0590
0930
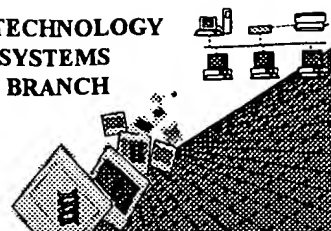
BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

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OIPE

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/901,572

DATE: 10/01/2002
TIME: 16:12:31

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10012002\I901572.raw**

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     3 <110> APPLICANT: Nippon Zeon Co., Ltd.,
W--> 4 <120> TITLE OF INVENTION: Modified DNA molecules, Recombinants and uses thereof
W--> 5 <130> FILE REFERENCE: J209
W--> 6 <140> CURRENT APPLICATION NUMBER:
C--> 7 <141> CURRENT FILING DATE: 2002-09-23
E--> 8 <160> NUMBER OF SEQ ID NOS:
     9 <170> SOFTWARE: PatentIn Ver. 2.1
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→ mandatory response needed
only 4 sequences in submitted file

Does Not Comply
Corrected Diskette Needed
see pp 1-4, 8

ERRORED SEQUENCES

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     10 <210> SEQ ID NO: 1
     11 <211> LENGTH: 1306
     12 <212> TYPE: DNA
     13 <213> ORGANISM: Mycoplasma gallisepticum
     14 <223> OTHER INFORMATION: TTM-1 gene
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     17 aatcctaaat aaataagccg ttaaattaac taaaaaatta aaaaaatggt ttttcttatc  120
     18 aaccaaaatt ctctagtaat aaacgcttat ttatttttat ttttagtcat cttttaagat  180
     19 ataaatatat cttaatattc tatgaataag aaaagaatca tcttaaagac tattagtttg  240
     20 ttaggtacaa catcctttct tagcattggg atttctagct gtatgtctat tactaaaaaa  300
     21 gatgcaaacc caaataatgg ccaaacccaa ttagaagcag cgcgaatgga gttaacagat  360
     22 ctaatcaatg ctaaagcgat gacattagct tcactacaag actatgccaa gattgaagct  420
     23 agtttatcat ctgcttatag tgaagctgaa acagttaaca ataaccttaa tgcaacatta  480
     24 gaacaactaa aaatggctaa aactaattta gaatcagcca tcaaccaagc taatacggat  540
     25 aaaacgactt ttgataatga acacccaaat ttagttgaag catacaaagc actaaaaacc  600
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     27 cgcaataatt tagtggatct atacaataaa gctagtagtt taataactaa aacactagat  720
     28 ccactaaatg ggggaacgct tttagattct aatgagatta ctacagttaa tcggaatatt  780
     29 aataatacgt tatcaactat taatgaacaa aagactaatg ctgatgcatt atctaatagt  840
     30 tttattaaaa aagtgattca aaataatgaa caaagttttg tagggacttt tacaaacgct  900
     31 aatgttcaac cttcaaacta cagtttt tgtt gctttt agtg ctgatgtaac acccgtcaat  960
     32 tataaatatg caagaaggac cgtttggaat ggtgatgaac cttcaagtag aattcttgca 1020
     33 aacacgaata gtatcacaga tgtttcttgg atttatagtt tagctggaac aaacacgaag 1080
     34 taccaattta gttttagcaa ctatggtcca tcaactggtt atttatattt cccttataag 1140
     35 ttggttaaag cagctgatgc taataacgtt ggattacaat acaaattaaa taatggaaat 1200
     36 gttcaacaag ttgagtttgc cacttcaact agtgcaaata atactacagc taatccaact 1260
     37 ccagcagttg atgagattaa agttgctaaa atcgttttat caggtt             1306
     38 <210> SEQ ID NO: 2
     39 <211> LENGTH: 3189
     40 <212> TYPE: DNA
     41 <213> ORGANISM: Mycoplasma gallisepticum
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→ <220> insert this mandatory numeric identifier whenever <221>, <222> or <223> is shown

FYI: Per 1,823 d) Sequence Rules, "a fixed-width font should be used exclusively throughout the 'Sequence Listing'": do not vary the font in the file 10/1/02

p.2

RAW SEQUENCE LISTING   DATE: 10/01/2002
PATENT APPLICATION: US/09/901,572   TIME: 16:12:31

Input Set : A:\EP.txt
· Output Set: N:\CRF4\10012002\I901572.raw
(2207)←insert
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     42 <223> OTHER INFORMATION: mgc3 gene
E--> 43 <400> SEQUENCE: 2
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     45 gctcttggtt ctgcaagctt tggctttaag caatcagata agagtaacga taacacgcaa  120
     46 ttagttaatc aagcaagaac gctagatgct aattctgtta gacttgcagg tcttggacaa  180
     47 aatggttcgt tgttcaatac agttcttaga gatgttgatg ataactttat aacagcagct  240
     48 aatggaacaa ttatcaaatt agatagtttt actaaaccat tatatggttt agatctaagt  300
     49 gatgattgtg gtggatacaa agtaaaacaa atagtttcag attacacaac tagcagaaat  360
     50 agatttgatc aaagacaaac aagagcatat tatgctctgt tggttaatga tgaagctaac  420
     51 gttcatttaa aaagaattaa tactaactca aatagaattg gtaatagaaa caacaattct  480
     52 aagtttgtaa ttggtggtgt tgataatcca gctcacgtaa ttagatttac tgatgatggg  540
     53 actaaattta attttacaaa ccaaactcaa ggtgaaattg ttaatgactt cattttagat  600
     54 gcgccaatct tacctaaaga tttacaccca gattggtata acttatacat tcaaagaaag  660
     57 atcttaccaa atgacgtcaa cactgcagtt gttccttggc cagtaggtag agttagtgga  720
     58 acaaatgctg atgatgggat gtttgattgt gggaatggtc aaataactaa tacagatcct  780
     59 attgctcaaa ctaaaaccac tactgataat caaaatcctt caacttttaa ttcaggagca  840
     60 atgcctggtg caaacaatag atacgattct caattgaatg tcaagcatag aattaaaaca  900
     61 tctttccaat tagatgaaaa atttgtttat ccagaatgga ctggttctga agagaataaa  960
     62 aatattacaa gattagctac tggaagtttg ccaagcaacg aaagatattg gattcttgac 1020
     63 atacccggga ctccacaagt tactttaaaa gaagattcag ttaacgtatt ttcaagacta 1080
     64 tacttaaact cagttaattc tttatcattc attggtgata gtatttatat ttttggtacc 1140
     65 tctgaattac catcattatg gtactattca ttcccaacta gattatctga tctaaccgct 1200
     66 ttgaatcaag ttaaaacaga tgatattgaa gcttcaagca ctgataacgg tacaacaaca 1260
     67 aacggaacaa cgacaacagc tgatacatct agtggttcaa caggtgctgg aacaggaaat 1320
     68 actactaaca cttctcaaac agtttctaat cctactttaa atacttatcg tagttttgga 1380
     69 attgatagta aaccaacttc tgcaaacaaa atagatgaaa ctaattgggc agatcctaac 1440
     70 gttattgaag caagaatata tgctgaatac agattaggta ttcaaaatga aattccaata 1500
     71 actaatgcag gaaactttat ccgaaacaca attggtggtg ttggtttttac ttcaacaggt 1560
     72 tcaagagtag ttttaagagc ttcttataac ggtgatcaac gtccaactgg aaacttccaa 1620
     73 cctttcttat acgtatttgg ttatttagga taccaacaaa ctagaacagg aactttctgg 1680
     74 tacggaacat ataagctttt aaacaacagc ccttacgacg tattagattc tccaagagta 1740
     75 ggtactgaaa ccaatcaatt tagaagaact tcattaacat accctgttat gggtggatat 1800
     76 ctaactgaag aaggtgctag aagtttctct aatactccat atataagagc acaaggtgac 1860
     77 acaccagaaa gccgaagcat cttccaatct ggctattctg ataatactta tgagtacatt 1920
     78 caatcagttt taggatttga tggaattaga aataacttaa atgttggggt taaagcatca 1980
     79 agcttcttaa actcaaatag accaaatcca aacggtctag aaatgattgc tgcaacaaca 2040
     80 tacttaagat cacaaattgg attagctaga acatctggat taccaaacca acaaccattc 2100
     81 ggaacaactc accaagttat ttcagtatca cctggtgatc agttctcatc aattaagaat 2160
     82 attagaacaa tcttccctgg taaccagtta tggtacttct tattcacaaa tgaaaataat 2220
     83 aaatctagtg tttatacatt aagattagct gactcaagta accctgatgc gtcaagctca 2280
     84 ttcagtccaa caagtttaat tgacgttaat gaaattggtg taatcttacc tttattagac 2340
     85 aattcattct atacagtaaa tgctgctggt aatgttgcat tgttctcatc aaaccctggt 2400
     86 tctcctggat catatactgc tgtaaataca tttaatcaga acttatctga tattgctttt 2460
     87 gaaggttctg gtgctaagta tacatctgat ttctggggaa caatccaatt caaacccgat 2520
     88 gagtacttaa ttcaaaatgg gttcactagt caagtggcta gaaacttcgt tacaaaccaa 2580
     89 agcttcttaa acagtttagt tgacttcact cctgctaatg ctggtactaa ctaccgtgta 2640
     90 gtggttgatc ctgatggtaa tttaacaaac caaaacctac ctctaaaagt tcagatccaa 2700
     91 tacttagatg gtaagtatta tgatgctaaa ttaaagaaca ataatttagt aacattctct 2760
     92 tataacaact ttggcgcctt accttcatgg gtagtgccta cagcaattgg tagtacatta 2820
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RAW SEQUENCE LISTING   DATE: 10/01/2002
PATENT APPLICATION: US/09/901,572   TIME: 16:12:31

Input Set : A:\EP.txt
Output Set: N:\CRF4\10012002\I901572.raw

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    93 ggtattcttg caattatgat catcttagga ttagctatcg gtattccttt aagagctcaa 2880
    94 agaaaattac aagacaaagg gttcaaaaca acattcaaaa aagttgatac cttgactgct 2940
    95 gctgttggtt cagtttacaa gaagattatt acccaaactg ctaacgttaa gaaaaaacct 3000
    96 gctgctttag gtgctggtaa atctggtgat aagaaacctg ctgctgctgc taaacctgct 3060
    97 gctccagcta aaccatctgc accaaaagct agctcaccag ctaaaccaac tgggcctaaa 3120
    98 tctggtgcgc ctacaaaacc aactgctcct aagccagctg ctccaaaacc aaccgctccc 3180
    99 aaagaataa                                                          3189
E--> 100 <210> SEQ ID NO: 12
     101 <211> LENGTH: 456
     102 <212> TYPE: PRT
     103 <213> ORGANISM: Mycoplasma gallisepticum
     104 <223> OTHER INFORMATION: TTM-1 portion of pNZ40K-S
E--> 105 <400> SEQUENCE: 12
     106 Met His Tyr Phe Arg Arg Asn Cys Ile Phe Phe Leu Ile Val Ile Leu
     107  1               5                  10                  15
E--> 108 Tyr Gly Thr Asn Ser Ser Pro Ser Thr Gln Asn Val Thr Ser Arg Glu
     109          20              25                  30
     112 Val Val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu
     113          35              40                  45
     114 Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Phe Gly Cys
     115      50              55                  60
     116 Met Ser Ile Thr Lys Lys Asp Ala Asn Pro Asn Asn Gly Gln Thr Gln
     117  65              70                  75                  80
     118 Leu Glu Ala Ala Arg Met Glu Leu Thr Asp Leu Ile Asn Ala Lys Ala
     119              85                  90                  95
     120 Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala Lys Ile Glu Ala Ser Leu
     121          100             105                 110
     122 Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val Asn Asn Asn Leu Asn Ala
     123          115             120                 125
     124 Thr Leu Glu Gln Leu Lys Met Ala Lys Thr Asn Leu Glu Ser Ala Ile
     125      130             135                 140
     126 Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe Asp Asn Glu His Pro Asn
     127 145             150                 155                 160
     128 Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr Thr Leu Glu Gln Arg Ala
     129              165                 170                 175
     130 Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala Tyr Asn Gln Ile Arg Asn
     131              180                 185                 190
     132 Asn Leu Val Asp Leu Tyr Asn Lys Ala Ser Ser Leu Ile Thr Lys Thr
     133              195                 200                 205
     134 Leu Asp Pro Leu Asn Gly Gly Thr Leu Leu Asp Ser Asn Glu Ile Thr
     135      210             215                 220
     136 Thr Val Asn Arg Asn Ile Asn Asn Thr Leu Ser Thr Ile Asn Glu Gln
     137 225             230                 235                 240
     138 Lys Thr Asn Ala Asp Ala Leu Ser Asn Ser Phe Ile Lys Lys Val Ile
     139              245                 250                 255
     140 Gln Asn Asn Glu Gln Ser Phe Val Gly Thr Phe Thr Asn Ala Asn Val
     141              260                 265                 270
     142 Gln Pro Ser Asn Tyr Ser Phe Val Ala Phe Ser Ala Asp Val Thr Pro
     143          275             280                 285
```

```
144 Val Asn Tyr Lys Tyr Ala Arg Arg Thr Val Trp Asn Gly Asp Glu Pro
145     290             295             300
146 Ser Ser Arg Ile Leu Ala Asn Thr Asn Ser Ile Thr Asp Val Ser Trp
147 305             310             315             320
148 Ile Tyr Ser Leu Ala Gly Thr Asn Thr Lys Tyr Gln Phe Ser Phe Ser
149             325             330             335
150 Asn Tyr Gly Pro Ser Thr Gly Tyr Leu Tyr Phe Pro Tyr Lys Leu Val
151             340             345             350
152 Lys Ala Ala Asp Ala Asn Asn Val Gly Leu Gln Tyr Lys Leu Asn Asn
153             355             360             365
154 Gly Asn Val Gln Gln Val Glu Phe Ala Thr Ser Thr Ser Ala Asn Asn
155     370             375             380
156 Thr Thr Ala Asn Pro Thr Pro Ala Val Asp Glu Ile Lys Val Ala Lys
157 385             390             395             400
158 Ile Val Leu Ser Gly Leu Arg Phe Gly Gln Asn Thr Ile Glu Leu Ser
159             405             410             415
160 Val Pro Thr Gly Glu Gly Asn Met Asn Lys Val Ala Pro Met Ile Gly
161             420             425             430
162 Asn Ile Tyr Leu Ser Ser Asn Glu Asn Asn Ala Asp Lys Ile Pro Gly
163             435             440             445
164 Tyr Arg Arg Pro Gly Thr Phe Leu
165     450             455
```

E--> 168 <210> SEQ ID NO: 25
     169 <211> LENGTH: 1224
     170 <212> TYPE: PRT
     171 <213> ORGANISM: Mycoplasma gallisepticum
     172 <223> OTHER INFORMATION: MGC3 encoded by mgc3 gene
E--> 173 <400> SEQUENCE: 25

```
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175   1             5             10             15
176 Ala Val Phe Gly Ala Leu Gly Ser Ala Ser Phe Gly Phe Lys Gln Ser
177             20             25             30
178 Asp Lys Ser Asn Asp Asn Thr Gln Leu Val Asn Gln Ala Arg Thr Leu
179             35             40             45
180 Asp Ala Asn Ser Val Arg Leu Ala Gly Leu Gly Gln Asn Gly Ser Leu
181     50             55             60
182 Phe Asn Thr Val Leu Arg Asp Val Asp Asp Asn Phe Ile Thr Ala Ala
183   65             70             75             80
184 Asn Gly Thr Ile Ile Lys Leu Asp Ser Phe Thr Lys Pro Leu Tyr Gly
185             85             90             95
186 Leu Asp Leu Ser Asp Asp Cys Gly Gly Tyr Lys Val Lys Gln Ile Val
187             100             105             110
188 Ser Asp Tyr Thr Thr Ser Arg Asn Arg Phe Asp Gln Arg Gln Thr Arg
189             115             120             125
190 Ala Tyr Tyr Ala Leu Leu Val Asn Asp Glu Ala Asn Val His Leu Lys
191     130             135             140
192 Arg Ile Asn Thr Asn Ser Asn Arg Ile Gly Asn Arg Asn Asn Asn Ser
193 145             150             155             160
194 Lys Phe Val Ile Gly Gly Val Asp Asn Pro Ala His Val Ile Arg Phe
```

[handwritten annotations:] → Seqs 13 through 24 missing (see p. 8)

[handwritten annotation near line 171:] → 1220? insert

RAW SEQUENCE LISTING   DATE: 10/01/2002
PATENT APPLICATION: US/09/901,572   TIME: 16:12:31

Input Set : A:\EP.txt
Output Set: N:\CRF4\10012002\I901572.raw

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197             180             185                 190
198 Ile Val Asn Asp Phe Ile Leu Asp Ala Pro Ile Leu Pro Lys Asp Leu
199         195             200                 205
200 His Pro Asp Trp Tyr Asn Leu Tyr Ile Gln Arg Lys Ile Leu Pro Asn
201     210             215                 220
202 Asp Val Asn Thr Ala Val Val Pro Trp Pro Val Gly Arg Val Ser Gly
203 225             230                 235                 240
204 Thr Asn Ala Asp Asp Gly Met Phe Asp Cys Gly Asn Gly Gln Ile Thr
205             245             250                 255
206 Asn Thr Asp Pro Ile Ala Gln Thr Lys Thr Thr Thr Asp Asn Gln Asn
207             260             265                 270
208 Pro Ser Thr Phe Asn Ser Gly Ala Met Pro Gly Ala Asn Asn Arg Tyr
209         275             280                 285
210 Asp Ser Gln Leu Asn Val Lys His Arg Ile Lys Thr Ser Phe Gln Leu
211     290             295                 300
212 Asp Glu Arg Ile Asn Thr Asn Ser Asn Arg Ile Gly Asn Arg Asn Asn
213 305·            310                 315                 320
214 Asn Ser Lys Phe Val Ile Gly Gly Val Asp Asn Pro Ala His Val Ile
215             325             330                 335
216 Arg Phe Thr Asp Asp Gly Thr Lys Phe Asn Phe Thr Asn Gln Thr Gln
217             340             345                 350
218 Gly Glu Ile Val Asn Asp Phe Ile Leu Asp Ala Pro Ile Leu Pro Lys
219         355             360                 365
220 Asp Leu His Pro Asp Trp Tyr Asn Leu Tyr Ile Gln Arg Lys Ile Leu
221     370             375                 380
224 Pro Asn Asp Val Asn Thr Ala Val Val Pro Trp Pro Val Gly Arg Val
225 385             390                 395                 400
226 Ser Gly Thr Asn Ala Asp Asp Gly Met Phe Asp Cys Gly Asn Gly Gln
227             405             410                 415
228 Ile Thr Asn Thr Asp Pro Ile Ala Gln Thr Lys Thr Thr Thr Asp Asn
229         ·420             425                 430
230 Gln Asn Pro Ser Thr Phe Asn Ser Gly Ala Met Pro Gly Ala Asn Asn
231         435             440                 445
232 Arg Tyr Asp Ser Gln Leu Asn Val Lys His Arg Ile Lys Thr Ser Phe
233     450             455                 460
234 Gln Leu Asp Glu Lys Phe Val Tyr Pro Glu Trp Thr Gly Ser Glu Glu
235 465             470                 475                 480
236 Asn Lys Asn Ile Thr Arg Leu Ala Thr Gly Ser Leu Pro Ser Asn Glu
237             485             490                 495
238 Arg Tyr Trp Ile Leu Asp Ile Pro Gly Thr Pro Gln Val Thr Leu Lys
239         500             505                 510
240 Glu Asp Ser Val Asn Val Phe Ser Arg Leu Tyr Leu Asn Ser Val Asn
241         515             520                 525
242 Ser Leu Ser Phe Ile Gly Asp Ser Ile Tyr Ile Phe Gly Thr Ser Glu
243     530             535                 540
244 Leu Pro Ser Leu Trp Tyr Tyr Ser Phe Pro Thr Arg Leu Ser Asp Leu
245 545             550                 555                 560
```

```
246 Thr Ala Leu Asn Gln Val Lys Thr Asp Asp Ile Glu Ala Ser Ser Thr
247                 565             570             575
248 Asp Asn Gly Thr Thr Thr Asn Gly Thr Thr Thr Ala Asp Thr Ser
249                 580             585             590
250 Ser Gly Ser Thr Gly Ala Gly Thr Gly Asn Thr Thr Asn Thr Ser Gln
251             595             600             605
252 Thr Val Ser Asn Pro Thr Leu Asn Thr Tyr Arg Ser Phe Gly Ile Asp
253     610             615             620
254 Ser Lys Pro Thr Ser Ala Asn Lys Ile Asp Glu Thr Asn Trp Ala Asp
255 625             630             635                     640
256 Pro Asn Val Ile Glu Ala Arg Ile Tyr Ala Glu Tyr Arg Leu Gly Ile
257             645             650             655
258 Gln Asn Glu Ile Pro Ile Thr Asn Ala Gly Asn Phe Ile Arg Asn Thr
259         660             665             670
260 Ile Gly Gly Val Gly Phe Thr Ser Thr Gly Ser Arg Val Val Leu Arg
261         675             680             685
262 Ala Ser Tyr Asn Gly Asp Gln Arg Pro Thr Gly Asn Phe Gln Pro Phe
263     690             695             700
264 Leu Tyr Val Phe Gly Tyr Leu Gly Tyr Gln Gln Thr Arg Thr Gly Thr
265 705             710             715                     720
266 Phe Trp Tyr Gly Thr Tyr Lys Leu Leu Asn Asn Ser Pro Tyr Asp Val
267             725             730             735
268 Leu Asp Ser Pro Arg Val Gly Thr Glu Thr Asn Gln Phe Arg Arg Thr
269             740             745             750
270 Ser Leu Thr Tyr Pro Val Met Gly Gly Tyr Leu Thr Glu Glu Gly Ala
271         755             760             765
272 Arg Ser Phe Ser Asn Thr Pro Tyr Ile Arg Ala Gln Gly Asp Thr Pro
273     770             775             780
274 Glu Ser Arg Ser Ile Phe Gln Ser Gly Tyr Ser Asp Asn Thr Tyr Glu
275 785             790             795                     800
276 Tyr Ile Gln Ser Val Leu Gly Phe Asp Gly Ile Arg Asn Asn Leu Asn
277             805             810             815
280 Val Gly Val Lys Ala Ser Ser Phe Leu Asn Ser Asn Arg Pro Asn Pro
281             820             825             830
282 Asn Gly Leu Glu Met Ile Ala Ala Thr Thr Tyr Leu Arg Ser Gln Ile
283         835             840             845
284 Gly Leu Ala Arg Thr Ser Gly Leu Pro Asn Gln Gln Pro Phe Gly Thr
285     850             855             860
286 Thr His Gln Val Ile Ser Val Ser Pro Gly Asp Gln Phe Ser Ser Ile
287 865             870             875                     880
288 Lys Asn Ile Arg Thr Ile Phe Pro Gly Asn Gln Leu Trp Tyr Phe Leu
289             885             890             895
290 Phe Thr Asn Glu Asn Asn Lys Ser Ser Val Tyr Thr Leu Arg Leu Ala
291         900             905             910
292 Asp Ser Ser Asn Pro Asp Ala Ser Ser Ser Phe Ser Pro Thr Ser Leu
293         915             920             925
294 Ile Asp Val Asn Glu Ile Gly Val Ile Leu Pro Leu Leu Asp Asn Ser
295     930             935             940
296 Phe Tyr Thr Val Asn Ala Ala Gly Asn Val Ala Leu Phe Ser Ser Asn
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RAW SEQUENCE LISTING   DATE: 10/01/2002
PATENT APPLICATION: US/09/901,572   TIME: 16:12:31

Input Set : A:\EP.txt
Output Set: N:\CRF4\10012002\I901572.raw

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298 Pro Gly Ser Pro Gly Ser Tyr Thr Ala Val Asn Thr Phe Asn Gln Asn
299             965        ·                970                975
300 Leu Ser Asp Ile Ala Phe Glu Gly Ser Gly Ala Lys Tyr Thr Ser Asp
301             980                985                990
302 Phe Trp Gly Thr Ile Gln Phe Lys Pro Asp Glu Tyr Leu Ile Gln Asn
303         995                 1000                 1005
304 Gly Phe Thr Ser Gln Val Ala Arg Asn Phe Val Thr Asn Gln Ser Phe
305     1010                1015                 1020
306 Leu Asn Ser Leu Val Asp Phe Thr Pro Ala Asn Ala Gly Thr Asn Tyr
307 1025                1030                1035                   1040
308 Arg Val Val Val Asp Pro Asp Gly Asn Leu Thr Asn Gln Asn Leu Pro
309             1045                1050                1055
310 Leu Lys Val Gln Ile Gln Tyr Leu Asp Gly Lys Tyr Tyr Asp Ala Lys
311         1060                1065                1070
312 Leu Lys Asn Asn Asn Leu Val Thr Phe Ser Tyr Asn Asn Phe Gly Ala
313     1075                1080                1085
314 Leu Pro Ser Trp Val Val Pro Thr Ala Ile Gly Ser Thr Leu Gly Ile
315     1090                1095                1100
316 Leu Ala Ile Met Ile Ile Leu Gly Leu Ala Ile Gly Ile Pro Leu Arg
317 1105                1110          ·        1115                 1120
318 Ala Gln Arg Lys Leu Gln Asp Lys Gly Phe Lys Thr Thr Phe Lys Lys
319             1125                1130                1135
320 Val Asp Thr Leu Thr Ala Ala Val Gly Ser Val Tyr Lys Lys Ile Ile
321         1140                1145                1150
322 Thr Gln Thr Ala Asn Val Lys Lys Lys Pro Ala Ala Leu Gly Ala Gly
323         1155                1160                1165
324 Lys Ser Gly Asp Lys Lys Pro Ala Ala Ala Ala Lys Pro Ala Ala Pro
325     1170                1175                1180
326 Ala Lys Pro Ser Ala Pro Lys Ala Ser Ser Pro Ala Lys Pro Thr Gly
327 1185                1190                1195                   1200
328 Pro Lys Ser Gly Ala Pro Thr Lys Pro Thr Ala Pro Lys Pro Ala Ala
329             1205                1210                1215
330 Pro Lys Pro Thr Ala Pro Lys Glu
331             1220
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/01/2002
PATENT APPLICATION: US/09/901,572   TIME: 16:12:32

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10012002\I901572.raw**

Skipped Sequences(NEW RULES):
Sequence(s)__missing. If intentional, please use the following format for
each skipped sequence.
<210> sequence id number
<400> sequence id number
000

Seq#:3,4,5,6,7,8,9,10,11,13,14,15,16,17,18,19,20,21,22,23,24

VERIFICATION SUMMARY   DATE: 10/01/2002
PATENT APPLICATION: US/09/901,572   TIME: 16:12:32

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10012002\I901572.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:283 W: Missing Blank Line separator, <140> field identifier
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:212 E: (34) Invalid or duplicate Sequence ID Number, Number Of Sequences Unknown
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:1
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:43 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:2
L:43 M:283 W: Missing Blank Line separator, <400> field identifier
L:100 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 3 thru 11
L:105 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:12
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:168 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 13 thru 24
L:173 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:25
L:173 M:283 W: Missing Blank Line separator, <400> field identifier
L:8 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (4)